

Figure 1A

1 CCACTGTGCTGGGAATTCGGCACGAGGCGAACGGACGTTTAAAGTGAGAAAAGAAACCGG 60

61 TAAATCAGAGATCCCAAGCAAGCGCGTGCCTGCATGATAGCGAAGAAAAAAGCTATCCG 120

121 TTTCAGTTAACTACTTACCAAGATTGAATTTTCGCCATCGGGCAAATTACTAAAAATACAT 180

181 AAGTGCAACTCGTCCACTGTGTGTTGTGTTTTTTTTTTTTTTTGGTTTCGCTGTGCC 240

241 TTTATCGCAAACAAGAACTGATAAACTAGAAAATATCTTGAGAAACTTGTTTTTCGCGCT 300

301 TTTCTTTTGCTAATTGCCGATCGCGGAAGAGAAAAACAAGCAGTAGACAAAACAAGTGTG 360

361 GTAATACAATCTGAAAAGGGCACCATCAGCAGCCCGAGGGGTTTATCTATATAGATGTGC 420

421 CAGCTTATCATCTCATGCTGTCTGTGAGGTGTCTGTGTGCTCGTGTAGTATCTTAAAT 480

481 ACATAGAGTGTGTTCATATAAAGTGCGACAAAGCTCGATTGGAAACAGCTGTGAGTGCC 540

541 CTTGAGTGGGTGGGCAAGATCGTCATCATCATCATCGTCGTCATTATCAACAGAATCAGC 600

601 ATCAGCATCTGGAGGCCCCGGATGCTCTAAGATCCCCAGTGTTTCATCAATTATGACTGCC 660

1 M T A 3

661 GAGACCTCAAGCCGTTTATAACGCCAACGAGTGCCAACGATGATGGTTTTCCGGCCAAA 720

4 E T L K P F I T P T S A N D D G F P A K 23

721 GCGACCAGCACGGCGACCGCCAGCGACGCACCCGCCAGCTGATCCCCCTGGTTTTGGGG 780

24 A T S T A T A Q R R T R Q L I P L V L G 43

781 TTCATCGGTCTGGGGCTGGTCGTTGCCATTCTCGCACTAACGATCTGGCAGACAACGCGT 840

44 F I G L G L V V A I L A L T I W Q T T R 63

841 GTATCGCATCTGGACAAGGAGCTGAAGAGCCTGAAGCGAGTCGTCGATAATCTCCAGCAG 900

64 V S H L D K E L K S L K R V V D N L Q Q 83

901 CGTTTGGGCATAAACTATCTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCC 960

84 R L G I N Y L D E F D E F Q K E Y E N A 103

961 CTCATCGACTATCCAAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGC 1020

104 L I D Y P K K V D G L T D E E D D D D G 123

Figure 1B

1021	GATGGTCTGGATTCCATTGCGGACGACGAGGACGACGACGTTAGCTATAGCTCTGTGGAT	1080
124	D G L D S I A D D E D D D V S Y S S V D	143
1081	GATGTTGGCGCAGACTACGAGGACTACACCGATATGTTAAATAAACTCAACAATGCACAT	1140
144	D V G A D Y E D Y T D M L N K L N N A H	163
1141	ACCGGCACCACGCCCACATCTGAGACCACTGCTGAGGGCGAGGGCGAGACGGACAGTGCA	1200
164	T G T T P T S E T T A E G E G E T D S A	183
1201	TCCTCAGCCTCAAATGATGACAATGTGTTGATGACTTTACCAGCTCAGATGCCCTCAAA	1260
184	S S A S N D D N V F D D F T S S D A L K	203
1261	AAGAAGCAGGAGAGAAAATCTCGCTCGATTGCCGATGTACGCAATGAGGAGCAGAATATT	1320
204	K K Q E R K S R S I A D V R N E E Q N I	223
1321	CAAGGAAATCACACAGAGCTTCAGGAAAAGTCATCCAATGAGGCAGCTTCCAAAGAGAGC	1380
224	Q G N H T E L Q E K S S N E A A S K E S	243
1381	CCTGCAGCACTTCACCTCCGTCGCAGAATGCATTCCCGCCATCGCCACCTCGTAGTCCGC	1440
244	P A A L H L R R R M H S R H R H L V V R	263
1441	AAAGCCAGATCCGAGGACTCGAGGCCAGCAGCCCATTTCCACTTGAGCAGCAGGCGGCGT	1500
264	K A R S E D S R P A A H F H L S S R R R	283
1501	CACCAAGAAAAGTATGGGCTACCATGGAGATATGTACATAGAAAATGATAGGGAGAGATGC	1560
284	H Q E S M G Y H G D M Y I E N D R E R C	303
1561	TCTTATCAGGGACACTTTCAAACGCGCGATGGCGTATTGACGGTGACCAATGCAGGCCTA	1620
304	S Y Q G H F Q T R D G V L T V T N A G E	323
1621	TATTACGTATACGCCCAGATATGGGGCTACAACTCGCACGACCAGAACGGATTTATCGTC	1680
324	Y V Y A Q E M G Y N S H D Q N G F I V	343
1681	TTTCAAGGAGACACTCCATTCTGTCAGTGCTTGAACACGGTGCCACCAACATGCCACAT	1740
344	F Q G D T P F L Q C L N T V P T N M P H	363
1741	AAGGTGCACACCTGCCACACGAGTGGTCTGATCCACCTGGAACGAAACGAGAGGATCCAT	1800
364	K V H T C H T S G L I H L E R N E R I H	383
1801	CTGAAGGACATTACAAACGATCGCAATGCAGTTCTGCGGGAGGGAACAACCGAAGCTAC	1860
384	L K D I H N D R N A V L R E G N N R S Y	403

Figure 2A

1	ATGACTGCCGAGACCCCTCAAGCCGTTTATAACGCCAACGAGTGCCAACGATGATGGTTTT	60
1	<u>M T A E T L K P F I T P T S A N D D G F</u>	20
61	CCGGCCAAAGCGACCAGCACGGCGACCGCCAGCGACGCACCCGCCAGCTGATCCCCCTG	120
21	<u>P A K A T S T A T A Q R R T R Q L I P L</u>	40
121	GTTTTGGGGTTCATCGGTCTGGGGCTGGTTCGTTGCCATTCTCGCACTAACGATCTGGCAG	180
41	<u>V L G F I G L G L V V A I L A L T I W Q</u>	60
181	ACAACGCGTGTATCGCATCTGGACAAGGAGCTGAAGAGCCTGAAGCGAGTCGTCGATAAT	240
61	T T R V S H L D K E L K S L K R V V D N	80
241	CTCCAGCAGCGTTTGGGCATAAACTATCTGGACGAGTTCGACGAGTTCCAAAAGGAGTAC	300
81	L Q Q R L G I N Y L D E F D E F Q K E Y	100
301	GAGAATGCCCTCATCGACTATCCAAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGAC	360
101	E N A L I D Y P K K V D G L T D E E D D	120
361	GACGATGGCGATGGTCTGGATTCCATTGCGGACGACGAGGACGACGACGTTAGCTATAGC	420
121	D D G D G L D S I A D D E D D D V S Y S	140
421	TCTGTGGATGATGTTGGCGCAGACTACGAGGACTACACCGATATGTTAAATAAACTCAAC	480
141	S V D D V G A D Y E D Y T D M L N K L N	160
481	AATGCACATACCGGCACCCACGCCCCACATCTGAGACCACTGCTGAGGGCGAGGGCGAGACG	540
161	N A H T G T T P T S E T T A E G E G E T	180
541	GACAGTGCATCCTCAGCCTCAAATGATGACAATGTGTTTCGATGACTTTACCAGCTACAAT	600
181	D S A S S A S N D D N V F D D F T S Y N	200
601	GCCCACAAAAAGAAGCAGGAGAGAAAAATCTCGCTCGATTGCCGATGTACGCAATGAGGAG	660
201	A H K K K Q E R K S R S I A D V R N E E	220
661	CAGAATATTCAAGGAAATCACACAGAGCTTCAGGAAAAGTCATCCAATGAGGCAACTTCC	720
221	Q N I Q G N H T E L Q E K S S N E A T S	240
721	AAAGAGAGAATGCATTCCCGCCATCGCCACCTCCTAGTCCGCAAAGGTGAATCTCTTCTT	780
241	K E R M H S R H R H L L V R K G E S L L	260
781	TCAGCCAGATCCGAGGACTCGAGGCCAGCAGCCCATTTCCACTTGAGCAGCAGGCGGCGT	840
261	S A R S E D S R P A A H F H L S S R R R	280
841	CACCAAGGAAGTATGGGCTACCATGGAGATATGTACATAGGAAATGATAACGAGAGAAAC	900
281	H Q G S M G Y H G D M Y I G N D N E R N	300

bioRxiv preprint doi: <https://doi.org/10.1101/111111>; this version posted January 1, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

Figure 2B

901 TCTTATCAGGGACACTTTCAAACGCGCGATGGCGTCTTGACGGTGACCAATACAGGCCTA 960
301 S Y Q G H F Q T R D G V [REDACTED] 320

961 TATTACGTATACGCCCAGATATGCTACAACAACTCGCACGACCAGAACGGATTTATCGTC 1020
321 [REDACTED] N N S H D Q N G F I V 340

1021 TTTCAAGGAGACACTCCATTCCTGCAGTGCTTGAACACGGTGCCCCACCAACATGCCACAT 1080
341 F Q G D T P F L Q C L N T V P T N M P H 360

1081 AAGGTGCACACCTGCCACACGAGTGGTCTGATCCACCTGGAACGAAACGAGAGGATCCAT 1140
361 K V H T C H T S G L I H L E R N E R I H 380

1141 CTGAAGGACATTCAACAACGATCGCAATGCAGTTCTGCGGGAGGGAAACAACCGAAGCTAC 1200
381 L K D I H N D R N A V L R E G N N R S Y 400

1201 TTTGGCATCTTCAAGGTGTAA 1221
401 F G I F K V 406

bioRxiv preprint doi: <https://doi.org/10.1101/123456>; this version posted January 1, 2018. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

Figure 3A

1 GGCACGAGGCGAACGGACGTTTAAAGTGAGAAAAGAAACCGGTAAATCAGAGATCCCAAG 60

61 CAAGCGCGTGCGTGCATGATAGCGAAGAAAAAAGCTATCCGTTTCAGTTAACTACTTAC 120

121 CAAGATTGAATTTTCGCCATCGGGCAAATTACTAAAAATACATAAGTGCAACTCGTCCACT 180

181 GTGTGTTGTGTTTTTTTTTTTTTTTTTTGGTTTTTCGCTGTGCCTTTATCGCAAACAAGAAC 240

241 TGATAAACTAGAAAATATCTTGAGAAACTTGTTTTTCGCGCTTTTCTTTTGCTAATTGCC 300

301 GATCGCGGAAGAGAAAAACAAGCAGTAGACAAAACAAGTGTGGTAATACAATCTGAAAAG 360

361 GGCACCATCAGCAGCCCGAGGGGTTTATCTATATAGATGTCGCAGCTTATCATCTCATGC 420

421 TGTCTGTGAGGTTGTTCTGTGTGCTCGTGTAAGTATCTTAAATACATAGAGTGTGTTTATA 480

481 TAAAGTGCACAAAGCTCGATTGGAAACAGCTGTGAGTGCCCTTGAGTGGGTGGGCAAG 540

541 ATCGTCATCATCATCATCGTCGTCATTATCAACAGAATCAGCATCAGCATCTGGAGGCCC 600

601 CGGTTGCTCTAAGATCCCCAGTGTTTCATCAATTATGACTGCCGAGACCCTCAAGCCGTTT 660

1 M T A E T L K P F 9

661 ATAACGCCAACGAGTGCCAACGATGATGGTTTTCCGGCCAAAGCGACCAGCACGGCGACC 720

10 I T P T S A N D D G F P A K A T S T A T 29

721 GCCCAGCGACGCACCCGCCAGCTGATCCCCCTGGTTTTGGGGTTCATCGGTCTGGGGCTG 780

30 A Q R R T R Q L I P L V L G F I G L G L 49

781 GTCGTTGCCATTCTCGCACTAACGATCTGGCAGACAACGCGTGTATCGCATCTGGACAAG 840

50 V V A I L A L T I W Q T T R V S H L D K 69

841 GAGCTGAAGAGCCTGAAGCGAGTCGTCGATAATCTCCAGCAGCGTTTGGGCATAAACTAT 900

70 E L K S L K R V V D N L Q Q R L G I N Y 89

901 CTGGACGAGTTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCATCGACTATCCAAAA 960

90 L D E F D E F Q K E Y E N A L I D Y P K 109

961 AAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGCGATGGTCTGGATTCCATT 1020

110 K V D G L T D E E D D D D G D G L D S I 129

Figure 3B

1021 GCGGACGACGAGGACGACGACGTTAGCTATAGCTCTGTGGATGATGTTGGCGCAGACTAC 1080
130 A D D E D D D V S Y S S V D D V G A D Y 149

1081 GAGGACTACACCGATATGTTAAATAAACTCAACAATGCACATACCGGCACCACGCCCACA 1140
150 E D Y T D M L N K L N N A H T G T T P T 169

1141 TCTGAGACCACTGCTGAGGGCGAGGGCGAGACGGACAGTGCATCCTCAGCCTCAAATGAT 1200
170 S E T T A E G E G E T D S A S S A S N D 189

1201 GACAATGTGTTTCGATGACTTTACCAGCTACAATGCCCCACAAAAAGAAGCAGGAGAGAAAA 1260
190 D N V F D D F T S Y N A H K K K Q E R K 209

1261 TCTCGCTCGATTGCCGATGTACGCAATGAGGAGCAGAATATTCAAGGAAATCACACAGAG 1320
210 S R S I A D V R N E E Q N I Q G N H T E 229

1321 CTTCAGGAAAAGTCATCCAATGAGGCAACTTCCAAAGAGAGCCCTGCACCACTTCACCAC 1380
230 L Q E K S S N E A T S K E S P A P L H H 249

1381 CGTCGCAGAATGCATTCCCGCCATCGCCACCTCCTAGTCCGCAAAGCCAGATCCGAGGAC 1440
250 R R R M H S R H R H L L V R K A R S E D 269

1441 TCGAGGCCAGCAGCCCATTTCCTACTTGAGCAGCAGGCGCGTCACCAAGGAAGTATGGGC 1500
270 S R P A A H F H L S S R R R H Q G S M G 289

1501 TACCATGGAGATATGTACATAGGAAATGATAACGAGAGAAACTCTTATCAGGGACACTTT 1560
290 Y H G D M Y I G N D N E R N S Y Q G H F 309

1561 CAAACGCGCGATGGCGTCTTGACGGTGACCAATACAGGCCTATATTACGTATACGCCCAG 1620
310 Q T R D G V D V I N T G I Y Y V Y A Q 329

1621 ATATGCTACAACAACTCGCACGACCAGAACGGATTTATCGTCTTTCAAGGAGACACTCCA 1680
330 E C Y N N S H D Q N G F I V F Q G D T P 349

1681 TTCCTGCAGTGCTTGAACACGGTGCCACCAACATGCCACATAAGGTGCACACCTGCCAC 1740
350 F L Q C L N T V P T N M P H K V H T C H 369

1741 ACGAGTGGTCTGATCCACCTGGAACGAAACGAGAGGATCCATCTGAAGGACATTACAAAC 1800
370 T S G L I H L E R N E R I H L K D I H N 389

1801 GATCGCAATGCAGTTCTGCGGGAGGGAAACAACCGAAGCTACTTTGGCATCTTCAAGGTG 1860
390 D R N A V L R E G N N R S Y F G I F K V 409

1861 TAAATTGGAGAGATTATCCCCGGTCAGAAGATGGAATACCAGTTTAAGCTTTTGTCCCCG 1920

1021 GCGGACGACGAGGACGACGACGTTAGCTATAGCTCTGTGGATGATGTTGGCGCAGACTAC 1080
 130 A D D E D D D V S Y S S V D D V G A D Y 149
 1081 GAGGACTACACCGATATGTTAAATAAACTCAACAATGCACATACCGGCACCACGCCCACA 1140
 150 E D Y T D M L N K L N N A H T G T T P T 169
 1141 TCTGAGACCACTGCTGAGGGCGAGGGCGAGACGGACAGTGCATCCTCAGCCTCAAATGAT 1200
 170 S E T T A E G E G E T D S A S S A S N D 189
 1201 GACAATGTGTTTCGATGACTTTACCAGCTACAATGCCCCACAAAAAGAAGCAGGAGAGAAAA 1260
 190 D N V F D D F T S Y N A H K K K Q E R K 209
 1261 TCTCGCTCGATTGCCGATGTACGCAATGAGGAGCAGAATATTCAAGGAAATCACACAGAG 1320
 210 S R S I A D V R N E E Q N I Q G N H T E 229
 1321 CTTCAGGAAAAGTCATCCAATGAGGCAACTTCCAAAGAGAGCCCTGCACCACTTCACCAC 1380
 230 L Q E K S S N E A T S K E S P A P L H H 249
 1381 CGTCGCAGAATGCATTCCCGCCATCGCCACCTCCTAGTCCGCAAAGCCAGATCCGAGGAC 1440
 250 R R R M H S R H R H L L V R K A R S E D 269
 1441 TCGAGGCCAGCAGCCCATTTCCTACTTGAGCAGCAGGCGCGTCACCAAGGAAGTATGGGC 1500
 270 S R P A A H F H L S S R R R H Q G S M G 289
 1501 TACCATGGAGATATGTACATAGGAAATGATAACGAGAGAAACTCTTATCAGGGACACTTT 1560
 290 Y H G D M Y I G N D N E R N S Y Q G H F 309
 1561 CAAACGCGCGATGGCGTCTTGACGGTGACCAATACAGGCCTATATTACGTATACGCCCAG 1620
 310 Q T R D G V D V I N T G I Y Y V Y A Q 329
 1621 ATATGCTACAACAACTCGCACGACCAGAACGGATTTATCGTCTTTCAAGGAGACACTCCA 1680
 330 E C Y N N S H D Q N G F I V F Q G D T P 349
 1681 TTCCTGCAGTGCTTGAACACGGTGCCACCAACATGCCACATAAGGTGCACACCTGCCAC 1740
 350 F L Q C L N T V P T N M P H K V H T C H 369
 1741 ACGAGTGGTCTGATCCACCTGGAACGAAACGAGAGGATCCATCTGAAGGACATTACAAAC 1800
 370 T S G L I H L E R N E R I H L K D I H N 389
 1801 GATCGCAATGCAGTTCTGCGGGAGGGAAACAACCGAAGCTACTTTGGCATCTTCAAGGTG 1860
 390 D R N A V L R E G N N R S Y F G I F K V 409
 1861 TAAATTGGAGAGATTATCCCCGGTCAGAAGATGGAATACCAGTTTAAGCTTTTGTCCCCG 1920

Figure 3C

1921 CGACTGCTCGTGAATGCGATTCATCGCCAGCGTGAATCCATTAGTTCGTAGTACCTAGTC 1980
1981 TTAGTCACTCCAAACCTAATCTCAATCGGAATCGTGCATACTGCATTAGTCAGAAGACGG 2040
2041 AGGAAAATCATATTTATTTTGTATATACTCGTTCGACTCTAAAAAGTGAATAAAAATATA 2100
2101 TGTAGCTATTAAAAAAAAAAAAAAAAAAAAAAAAAAAACTCGAG 2148

bioRxiv preprint doi: <https://doi.org/10.1101/111111>; this version posted November 1, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

Figure 4

		1	50
DmTNF	(1)	MTAETLKPFITPTSANDDGFPAKATSTATAQRRTRQLIPLVLGFIGLGLV	
DmTNFv1	(1)	MTAETLKPFITPTSANDDGFPAKATSTATAQRRTRQLIPLVLGFIGLGLV	
DmTNFv2	(1)	MTAETLKPFITPTSANDDGFPAKATSTATAQRRTRQLIPLVLGFIGLGLV	
		51	100
DmTNF	(51)	VAILALTIWQTTRVSHLDKELKSLKRVVDNLQORLGINYLDEFDEFQKEY	
DmTNFv1	(51)	VAILALTIWQTTRVSHLDKELKSLKRVVDNLQORLGINYLDEFDEFQKEY	
DmTNFv2	(51)	VAILALTIWQTTRVSHLDKELKSLKRVVDNLQORLGINYLDEFDEFQKEY	
		101	150
DmTNF	(101)	ENALIDYPKKVDGLTDEEDDDGDGLDSIADDEDDDVSYSSVDDVGADYE	
DmTNFv1	(101)	ENALIDYPKKVDGLTDEEDDDGDGLDSIADDEDDDVSYSSVDDVGADYE	
DmTNFv2	(101)	ENALIDYPKKVDGLTDEEDDDGDGLDSIADDEDDDVSYSSVDDVGADYE	
		151	200
DmTNF	(151)	DYTDMLNKLNNHAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTSYN	
DmTNFv1	(151)	DYTDMLNKLNNHAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTSYN	
DmTNFv2	(151)	DYTDMLNKLNNHAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTSYN	
		201	250
DmTNF	(201)	AHKKKQERKRSRSIADVRNEEQNIQGNHTELOEKSSNEATSKESPAALHLR	
DmTNFv1	(201)	AHKKKQERKRSRSIADVRNEEQNIQGNHTELOEKSSNEATSKESPAALHLR	
DmTNFv2	(201)	AHKKKQERKRSRSIADVRNEEQNIQGNHTELOEKSSNEATSKESPAALHLR	
		251	300
DmTNF	(251)	RRMHSRHRHLVVRK-----ARSEDSRPAAHFHLSSRRRHQESMGYHGDM	
DmTNFv1	(243)	-RMHSRHRHLVVRKGESLLSARSEDSRPAAHFHLSSRRRHQESMGYHGDM	
DmTNFv2	(251)	RRMHSRHRHLVVRK-----ARSEDSRPAAHFHLSSRRRHQESMGYHGDM	
		301	350
DmTNF	(295)	YTGNDNERNSYQGHFQTRDGVLTVTNGLYVVYAQICYNNSHDQNGFIVF	
DmTNFv1	(292)	YTGNDNERNSYQGHFQTRDGVLTVTNGLYVVYAQICYNNSHDQNGFIVF	
DmTNFv2	(295)	YTGNDNERNSYQGHFQTRDGVLTVTNGLYVVYAQICYNNSHDQNGFIVF	
		351	400
DmTNF	(345)	QGDTPFLQCLNTVPTNMPHKVHTCHTSGLIHLERNERIHLKDIHNDRNAV	
DmTNFv1	(342)	QGDTPFLQCLNTVPTNMPHKVHTCHTSGLIHLERNERIHLKDIHNDRNAV	
DmTNFv2	(345)	QGDTPFLQCLNTVPTNMPHKVHTCHTSGLIHLERNERIHLKDIHNDRNAV	
		401	415
DmTNF	(395)	LREGNNRSYFGIFKV	
DmTNFv1	(392)	LREGNNRSYFGIFKV	
DmTNFv2	(395)	LREGNNRSYFGIFKV	

Figure 5

AC005974 : DS05033 (P1 D347), DS01913 (P1 D350). Finished; 158983 bases.
Length = 158,983

Minus Strand HSPs:

Score = 77 (27.1 bits), Expect = 5.5, P = 1.0
Identities = 20/58 (34%), Positives = 31/58 (53%), Frame = -1

Query: 203 NGKLIV**QDGFYYLYANIC**FRH-HETSGDLA---TEYLQLMVYV-TKTSIKIPSSHT 254
+G L V G YY+YA IC+ + H+ +G + T +LQ + V T K+ + HT
Sbjct: 129394 DGVLT**VTNTGLYYVYAQIC**YNNSHDQNGFIVFQDTPFLQCLNTVPTNMPHKVHTCHT
129221

Score = 45 (15.8 bits), Expect = 79., Sum P(2) = 1.0
Identities = 9/17 (52%), Positives = 10/17 (58%), Frame = -1

Query: 28 GPLHAPP--PPAPHQPP 42
GP PP PP+P PP
Sbjct: 132361 GPSLPPPPPPPSERTPP 132311

Figure 5 shows two sequence alignments. The first alignment is between a query sequence (NGKLIVQDGFYYLYANICFRH-HETSGDLA---TEYLQLMVYV-TKTSIKIPSSHT) and a subject sequence (DGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQDTPFLQCLNTVPTNMPHKVHTCHT). The second alignment is between a query sequence (GPLHAPP--PPAPHQPP) and a subject sequence (GPSLPPPPPPPSERTPP). Both alignments show high identity and positive scores, indicating strong sequence similarity.

[illegible][illegible]

Figure 6B

		301		350
DmTNF	(272)	PAAHFLSSRRRHQESMGYHCDMYIENDRER-CSYQGHEQTRDGVLTVTN		
DmTNFv1	(269)	PAAHFLSSRRRHQESMGYHCDMYIGNDNER-NSYQGHEQTRDGVLTVTN		
DmTNFv2	(272)	PAAHFLSSRRRHQESMGYHCDMYIGNDNER-NSYQGHEQTRDGVLTVTN		
Osteoprotegerin	(165)	--FAHLTINATDIPSG-SHKVSLSSWYHDRG-WAKTSNMTFSNCKLIINQ		
hCD27L	(53)	--LGWDVAELQLNHTGPDQDPRVWQGGPALGRSFLHGPGLKQQLRIHR		
hCD30L	(86)	LLCILKRAPPFKKSWAYLQVAKHLNKTCLSWNKDGLHGMRYQDGNLVIQF		
hTRAIL	(131)	-GRSN-TLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLNCELVIHE		
hEctodysplasmin_A	(249)	AVVHLQGGGSAIQVKNLDSGGVINDWSRITM-NPKVFKLHPRSCLEVLV		
mEctodysplasmin_A	(249)	AVVHLQGGGSAIQVKNLDSGGVINDWSRITM-NPKVFKLHPRSCLEVLV		
		351		400
DmTNF	(321)	AGLYYVY-----AQTWGYNSHDONGFIVFQG-DTPFLQCLNTVPTNM		
DmTNFv1	(318)	TGLYYVY-----AQTCYNNSHDONGFIVFQG-DTPFLQCLNTVPTNM		
DmTNFv2	(321)	TGLYYVY-----AQTCYNNSHDONGFIVFQG-DTPFLQCLNTVPTNM		
Osteoprotegerin	(211)	DGYVYLYANICFRHETSGDLATEYLOLMVYVTKTSIKTPSSHTLMKGGG		
hCD27L	(101)	DGIYMHITQVTLAICSSITASRHHPITLAVGICS---PASRSTSLRLSF		
hCD30L	(136)	PGLYFLICQLQFLVQCPNNSVDLKELELLINKHIKKQALVTVCESQMOTKH		
hTRAIL	(179)	KGEVYLYSQTYFRFQEEIKENTKNOKOMVOYTYK-YTSYPPDLLMK SAR		
hEctodysplasmin_A	(298)	DGTVEFLYSQ-----VEVYYINFTEFASVEVVVD-EKPFLOCTRSIETGK		
mEctodysplasmin_A	(298)	DGTVEFLYSQ-----VEVYYINFTEFASVEVVVD-EKPFLOCTRSIETGK		
		401		450
DmTNF	(362)	PHK-----VHTCHTSGLIHLERNERIHLDKTHMNRNAVIREGNRNSY		
DmTNFv1	(359)	PHK-----VHTCHTSGLIHLERNERIHLDKTHMNRNAVIREGNRNSY		
DmTNFv2	(362)	PHK-----VHTCHTSGLIHLERNERIHLDKTHMNRNAVIREGNRNSY		
Osteoprotegerin	(261)	TKYWSGNSEHFHYSINVCGEFKLRSCEHISIEVSNPSILDPDQ---DATY		
hCD27L	(148)	HQG-----CTIVSQRITPLARGDTLCTNLGTLLPSRNT---DETF		
hCD30L	(186)	VYQN-----LSQFLLDYLOVNTTISVNVDTFOYIDTSTFPLENVL		
hTRAIL	(228)	NSCWSKDAEYGLYSINOCGIFELKENDRIFVSVTNEHLIDMDH---EASE		
hEctodysplasmin_A	(341)	TN-----YNTCYTAGVCLLKAROKIAVKMVHADISINMS--KHTTE		
mEctodysplasmin_A	(341)	TN-----YNTCYTAGVCLLKAROKIAVKMVHADISINMS--KHTTE		
		451		462
DmTNF	(404)	FGIFKVV-----		
DmTNFv1	(401)	FGIFKVV-----		
DmTNFv2	(404)	FGIFKVV-----		
Osteoprotegerin	(308)	FGAFKVRDID--		
hCD27L	(186)	FGVQWVRP----		
hCD30L	(226)	SIFLYSNSD---		
hTRAIL	(275)	FGAFLVG-----		
hEctodysplasmin_A	(380)	FGAIRLGEAPAS		
mEctodysplasmin_A	(380)	FGAIRLGEAPAS		

Figure 6B shows the alignment of the DmTNF, DmTNFv1, DmTNFv2, Osteoprotegerin, hCD27L, hCD30L, hTRAIL, hEctodysplasmin_A, and mEctodysplasmin_A proteins. The alignment is shown in three blocks, with the first block showing the N-terminal region (residues 301-350), the second block showing the middle region (residues 351-400), and the third block showing the C-terminal region (residues 401-450). The alignment is shown in a table format, with the protein names and residue numbers in the first column, and the amino acid sequences in the subsequent columns. The sequences are aligned based on their homology, with gaps indicated by dashes. The alignment shows that the DmTNF, DmTNFv1, and DmTNFv2 proteins are highly similar to each other, while the Osteoprotegerin, hCD27L, hCD30L, hTRAIL, hEctodysplasmin_A, and mEctodysplasmin_A proteins show more variation in their sequences.

Figure 7

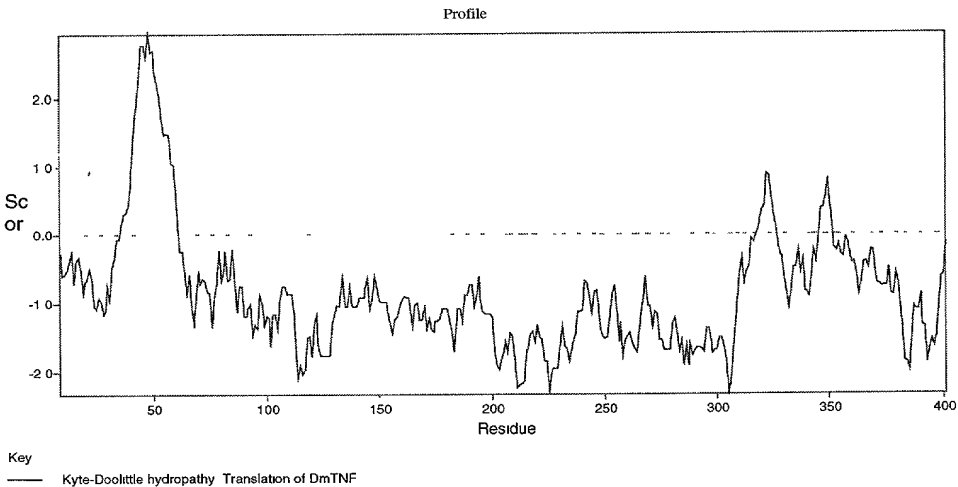


Figure 8

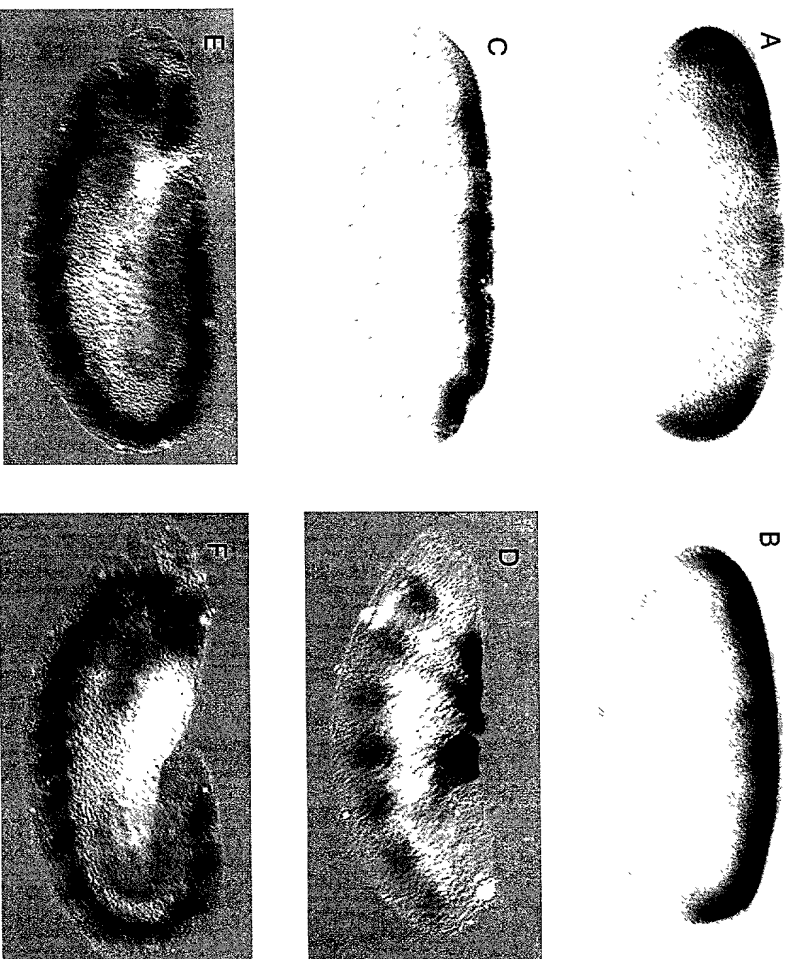


Figure 8 shows the development of a C. elegans embryo. Panel A shows a single-cell embryo. Panel B shows a two-cell embryo. Panel C shows a four-cell embryo. Panel D shows an eight-cell embryo. Panel E shows a morula stage embryo.

Figure 9

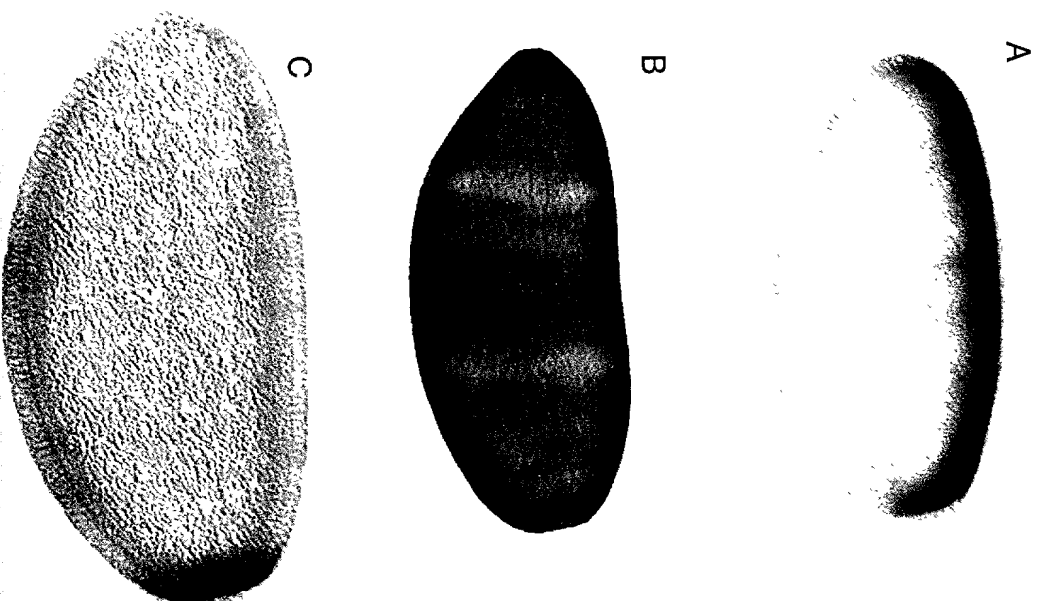


Figure 9 shows three different types of cells. The top cell (A) is a large, oval-shaped cell with a dark, irregular border. The middle cell (B) is a smaller, oval-shaped cell with a dark, irregular border. The bottom cell (C) is a large, oval-shaped cell with a dark, irregular border.

Figure 10

Expression profile of *Drosophila* TNF during development

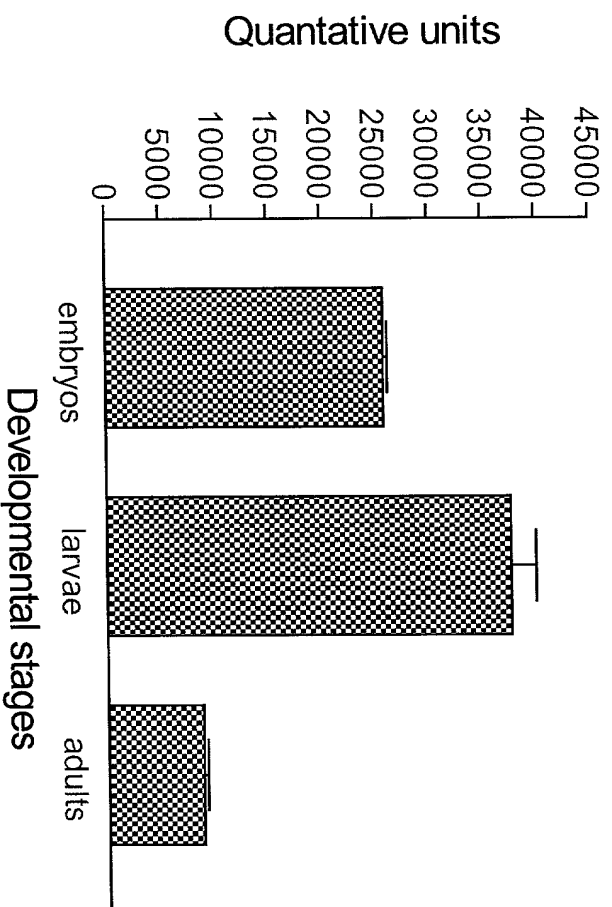


Figure 11

DmTNF

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human osteoprotegerin protein	gil12643360	21.4%	35.7%
human hCD27 ligand protein	gil P32970	12.5%	37.5%
human CD30 ligand protein	gil P32971	20%	26.7%
human TRAIL protein	gil P50591	24.6%	34.4%
human ectodysplasmin_A protein	gilQ92838	21.2%	27.9%
mouse ectodysplasmin_A protein	gilNP_034229	20.4%	28.5%

DmTNFv1

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human osteoprotegerin protein	gil12643360	23.8%	30.5%
human hCD27 ligand protein	gil P32970	12.5%	37.5%
human CD30 ligand protein	gil P32971	20%	26.7%
human TRAIL protein	gil P50591	23.3%	32.7%
human ectodysplasmin_A protein	gilQ92838	21.8%	28.6%
mouse ectodysplasmin_A protein	gilNP_034229	21%	28.6%

DmTNFv2

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human osteoprotegerin protein	gil12643360	21.4%	35.7%
human hCD27 ligand protein	gil P32970	12.5%	37.5%
human CD30 ligand protein	gil P32971	20%	26.7%
human TRAIL protein	gil P50591	24.1%	33.9%
human ectodysplasmin_A protein	gilQ92838	22.4%	29.1%
mouse ectodysplasmin_A protein	gilNP_034229	21.6%	29.2%

Figure 12

